IN THE CLAIMS

Amend the claims as follows.

1. (Currently Amended) A computer assisted method of providing a personalized lifestyle advice plan for a human subject comprising:

(i)   providing a first dataset on a data processing device ~~means~~, said first dataset comprising information correlating the presence of individual alleles at genetic loci, wherein at least one allele of each genetic locus known to be associated with increased or decreased disease susceptibility, with a lifestyle risk factor, ~~wherein at least one allele of each genetic locus is known to be associated with increased or decreased disease susceptibility~~;

(ii)   providing a second dataset on a data processing device~~means~~, said second dataset comprising information matching each said risk factor with at least one lifestyle recommendation;

(iii)   inputting a third dataset identifying alleles at one or more of the genetic loci of said first dataset of said human subject;

(iv)   determining the risk factors associated with said alleles of said human subject using said first dataset;

(v)   determining at least one ~~appropriate~~ lifestyle recommendation based on each identified risk factor from step (iv) using said second dataset; and

(vi) generating a personalized lifestyle advice plan based on said lifestyle recommendations.

2. (Currently Amended) The method according to ~~the method of~~ claim 1 wherein the personalised lifestyle advice plan includes recommended minimum and/or maximum amounts of food subtypes.

3. (Original) The method according to claim 1 or claim 2 wherein the method comprises the step of delivering the report to the client.

4. (Original) The method according to claim 3 wherein the plan is delivered via the Internet and accessible via a unique identifier code.

5. (Original) The method according to claim 4 wherein the plan comprises hyperlinks to one or more Web pages.

6. (Original) The method according to claim 1 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of genes selected from the group comprising:

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(a) genes that encode enzymes responsible for detoxification of xenobiotics in Phase I metabolism;

(b) genes that encode enzymes responsible for conjugation reactions in Phase II metabolism;

(c) genes that encode enzymes that help cells to combat oxidative stress;

(d) genes associated with micronutrient deficiency; and

(e) genes that encode enzymes responsible for metabolism of alcohol.

(f) genes that encode enzymes involved in lipid and/or cholesterol metabolism;

(g) genes that encode enzymes involved in clotting;

(h) genes that encode trypsin inhibitors;

(i) genes that encode enzymes related to susceptibility to metal toxicity;

(j) genes which encode proteins required for normal cellular metabolism and growth;

(k) genes which encoded HLA Class 2 molecules.

7. (Original) The method according to claim 6 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of genes selected from each member of the group comprising:

(a) genes that encode enzymes responsible for detoxification of xenobiotics in Phase I metabolism;

(b) genes that encode enzymes responsible for conjugation reactions in Phase II metabolism;

(c) genes that encode enzymes that help cells to combat oxidative stress;

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(d) genes associated with micronutrient deficiency; and

(e) genes that encode enzymes responsible for metabolism of alcohol.

(f) genes that encode enzymes involved in lipid and/or cholesterol metabolism;

(g) genes that encode enzymes involved in clotting;

(h) genes that encode trypsin inhibitors;

(i) genes that encode enzymes related to susceptibility to metal toxicity;

(j) genes which encode proteins required for normal cellular metabolism and growth;

(k) genes which encoded HLA Class 2 molecules.

8. (Original) The method according to claim 6 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of genes encoding an enzyme selected from the group comprising: cytochrome P450 monooxygenase, N-acetyltransferase 1 , N-acetyltransferase 2, glutathione-S– transferase, manganese superoxide dismutase, 5,10-methylenetetrahydrofolatereductase and alcohol dehydrogenase 2.

9. (Original) The method according to claim 8 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of each of the genes encoding cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S–transferase, manganese superoxide dismutase, 5,10-methylene-tetrahydrofolatereductase and alcohol dehydrogenase 2.

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10. (Original) The method according to claim 1 including the step of determining the presence of individual alleles at one or more genetic loci of the DNA in a DNA sample of said human subject, and constructing the dataset used in step (iii) using results of said determination.

11. (Original) The method according to claim 10 wherein said presence of said individual alleles is determined by hybridisation with allele-specific oligonucleotides.

12. (Original) The method according to claim 11 wherein said allele specific oligonucleotides are selected from oligonucleotides each specific for one of the genes selected from the group comprising the CYP1A1 gene, the GSTμ gene, the GSTπ gene, the GSTθ gene, the NAT1 gene, the NAT2 gene, the MnSOD gene, the MTHFR gene and the ALDH2 gene.

13 (Currently Amended) The method of claim 9 wherein said alleles are alleles of ~~the genes of the~~ genes selected from the group consisting of the MTHFR gene, the MnSOD gene, the CYP1A1 gene, the GSTμ gene, the GSTπ gene, the GSTθ gene and the ALDH2 gene.

14. (new) A computer assisted method of providing a personalized lifestyle advice plan for a human subject comprising:

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(i)   providing a first dataset on a data processing device, said first dataset comprising information correlating the presence of individual alleles at genetic loci, wherein at least one allele of each genetic locus known to be associated with increased or decreased disease susceptibility, with a lifestyle risk factor;

(ii)   providing a second dataset on a data processing device, said second dataset comprising information matching each said risk factor with at least one lifestyle recommendation;

(iii)   inputting a third dataset identifying alleles at two or more of the genetic loci of said first dataset of said human subject;

(iv)   determining the risk factors associated with said alleles of said human subject using said first dataset;

(v)   determining at least one lifestyle recommendation based on each identified risk factor from step (iv) using said second dataset; and

(vi) generating a personalized lifestyle advice plan based on said lifestyle recommendations.

15. (new) The method of claim 14 wherein the personalised lifestyle advice plan includes recommended minimum and/or maximum amounts of food subtypes.

16. (new) The method according to claim 14 or claim 15 wherein the method comprises the step of delivering the report to the client.

17. (new) The method according to claim 16 wherein the plan is delivered via the Internet and accessible via a unique identifier code.

18. (new) The method according to claim 17 wherein the plan comprises hyperlinks to one or more Web pages.

19. (new) The method according to claim 14 wherein said first dataset comprises information relating to two or more alleles of two or more genetic loci of genes selected from the group comprising:

(a) genes that encode enzymes responsible for detoxification of xenobiotics in Phase I metabolism;

(b) genes that encode enzymes responsible for conjugation reactions in Phase II metabolism;

(c) genes that encode enzymes that help cells to combat oxidative stress;

(d) genes associated with micronutrient deficiency; and

(e) genes that encode enzymes responsible for metabolism of alcohol.

(f) genes that encode enzymes involved in lipid and/or cholesterol metabolism;

(g) genes that encode enzymes involved in clotting;

(h) genes that encode trypsin inhibitors;

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(i) genes that encode enzymes related to susceptibility to metal toxicity;

(j) genes which encode proteins required for normal cellular metabolism and growth;

(k) genes which encoded HLA Class 2 molecules.

20. (new) The method according to claim 19 wherein said first dataset comprises information relating to two or more alleles of two or more genetic loci of genes selected from each member of the group comprising:

(a) genes that encode enzymes responsible for detoxification of xenobiotics in Phase I metabolism;

(b) genes that encode enzymes responsible for conjugation reactions in Phase II metabolism;

(c) genes that encode enzymes that help cells to combat oxidative stress;

(d) genes associated with micronutrient deficiency; and

(e) genes that encode enzymes responsible for metabolism of alcohol.

(f) genes that encode enzymes involved in lipid and/or cholesterol metabolism;

(g) genes that encode enzymes involved in clotting;

(h) genes that encode trypsin inhibitors;

(i) genes that encode enzymes related to susceptibility to metal toxicity;

(j) genes which encode proteins required for normal cellular metabolism and growth;

(k) genes which encoded HLA Class 2 molecules.

21. (new) The method according to claim 19 wherein said first dataset comprises information relating to two or more alleles of two or more genetic loci of genes encoding an enzyme selected from the group comprising: cytochrome P450 monooxygenase, N-acetyltransferase 1 , N-acetyltransferase 2, glutathione-S–transferase, manganese superoxide dismutase, 5,10-methylenetetrahydrofolatereductase and alcohol dehydrogenase 2.

22. (new) The method according to claim 21 wherein said first dataset comprises information relating to two or more alleles of two or more genetic loci of each of the genes encoding cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S–transferase, manganese superoxide dismutase, 5,10-methylene-tetrahydrofolatereductase and alcohol dehydrogenase 2.

23. (new) The method according to claim 14 including the step of determining the presence of individual alleles at two or more genetic loci of the DNA in a DNA sample of said human subject, and constructing the dataset used in step (iii) using results of said determination.

24. (new) The method according to claim 23 wherein said presence of said individual alleles is determined by hybridisation with allele-specific oligonucleotides.

25. (new) The method according to claim 24 wherein said allele specific oligonucleotides are selected from oligonucleotides each specific for two of the genes

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selected from the group comprising the CYP1A1 gene, the GSTμ gene, the GSTπ

gene, the GSTθ gene, the NAT1 gene, the NAT2 gene, the MnSOD gene, the MTHFR

gene and the ALDH2 gene.

26. (new) The method of claim 22 wherein said alleles are alleles of the genes

selected from the group consisting of the MTHFR gene, the MnSOD gene, the CYP1A1

gene, the GSTμ gene, the GSTπ gene, the GSTθ gene and the ALDH2 gene.

27. (new) The method of claim 1 wherein said first dataset and said second

dataset are provided on the same data processing device.

28. (new) The method of claim 14 wherein said first dataset and said second

dataset are provided on the same data processing device.

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